AMENDMENT TO THE SPECIFICATION

The paragraph numbers referred to below are those shown in the US PG-Pub No. 2007/0298032 of the present application.

Please replace paragraph [0017] (corresponding to page 5, third paragraph of the specification as the originally filed) with the following amended paragraph:

[**0017**] The ligand of the present invention preferably immunoreacts with LuxR or a homologue of LuxR between the negative regulation domain and the autoinducer-binding domain. In the case of LuxR, which is a polypeptide of 250 amino acids, the ligand preferably binds between amino acid residues 19 and 80, more preferably between amino acid residues 19 and 31. More preferably, the ligand employed in the invention immunoreacts with the amino acid sequence TCNNNKDINQC (SEQ ID NO: 1).

Please replace paragraph [0093] (corresponding to page 18, first paragraph of the specification as the originally filed) with the following amended paragraph:

[**0093**] FIG. **1** shows an alignment of LuxR homologues. Sequences (SEQ ID NO: 2 to SEQ ID NO: 16) aligned using the Clustal alignment algorithm included in the LaserGene sequence analysis package. Black=invariant residues. From: Stevens, A M & Greenberg, E P (1999) Transcriptional Activation by LuxR. In: Cell-Cell Signalling in Bacteria, Eds. Dunny, G M & Winans, S C, American Society for Microbiology p 238.

Please replace paragraph [0138] (corresponding to page 24, bottom paragraph of the specification as the originally filed) with the following amended paragraph:

[**0138**] A short synthetic peptide was produced on site in the Protein Science Facility according to the methods of Fields et al. (1990). The peptide sequence was chosen from a region close to the N-terminus of the luxR protein of *V. fischeri* strain ES114 (ATCC 700601). The sequence (SEQ ID NO: 1) is shown below.

N-terminal residue T C N N N K D I N Q C C-terminal residue